CIPHERGEN

ProteinChip® Software v3.0

QUICK START GUIDE

ProteinChip® Software Quick Start

Installation instructions

Preparing for installation

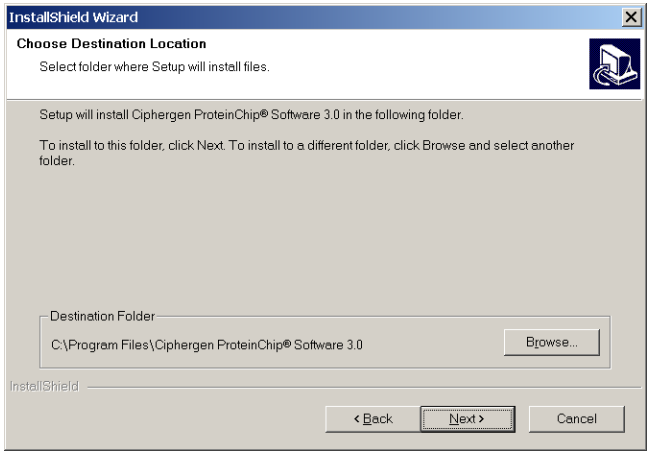
- Please note that Microsoft Windows NT 4.0 or Microsoft Windows 2000 is required to run Ciphergen ProteinChip® Software.
- Installation of the software will require administrator privileges on the computer you are installing the software on.
- Close all programs first to prevent installation conflicts.
- Although previous versions of ProteinChip Software (i.e. 2.x) can be present on the same computer, it is recommended that any previous versions of v3.0 be uninstalled before installing the newest software. See below for instructions.
- For the latest information, please review the *release.doc* file located on the installation CD.

Uninstalling previous versions of v3.0

1. Select the Control Panel from the Settings menu on the Windows Start button.
2. Select Add/Remove Programs.
3. Under the currently installed programs list, select Ciphergen ProteinChip® Software 3.0.
4. Click the Change/Remove button.
5. Select the Remove option and follow the rest of the InstallShield Wizard's steps.

Installing ProteinChip® Software v3.0

1. Browse the CD for the *setup.exe* icon, located in the "ProteinChip Software 3.0" folder.
2. Double-click the icon to launch the setup program.
3. Select the destination folder for the installation on the first page of the InstallShield Wizard. Please note that the default installation directory (previously "C:\SELDI") is now under "C:\Program Files\Ciphergen ProteinChip Software 3.0".



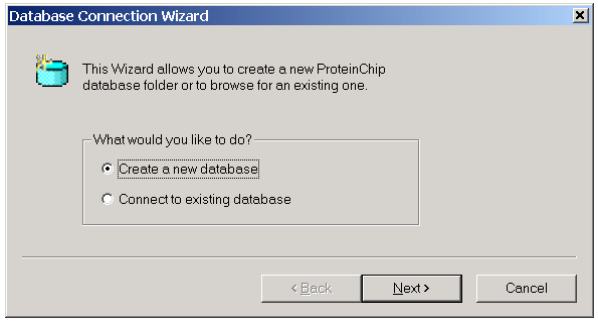
4 Follow the rest of the installation instructions, clicking Next to proceed.

5 ***Note**: Allow the software to restart the computer at the end of the installation process*. It is important to restart the computer, as the software may not function properly otherwise.

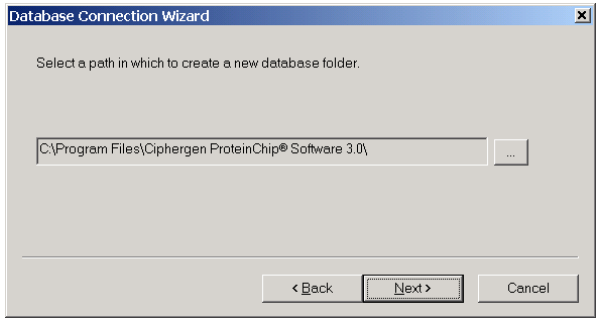
Initial start up

Creating a new Database

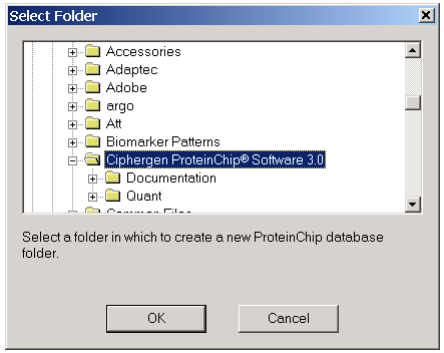
1 Launch the ProteinChip® Software by double-clicking on the desktop icon, or browsing through the Start Menu. After starting, the program will display the Database Connection Wizard, which will allow you to create a new ProteinChip database. If you are already logged into the software and would like to create a new database, select the **New | Database** item from the **File** menu.



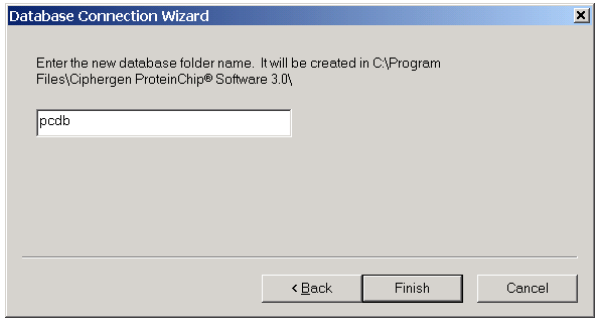
2 Select '**Create a new database**' and press the **Next** button. The second page of the wizard will be displayed, which will allow you to select the path for the new database folder. The program will default to the installation path that the ProteinChip software has been installed to.



3 Press the **…** button to browse to other directories using the **Select Folder** dialog. When the desired folder is selected, press the **Next** button.



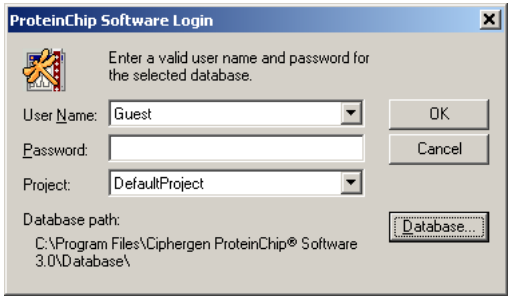
4 In the third page of the database wizard, enter the name of the folder to create that will contain the new ProteinChip database.



A message will appear after pressing the **Finish** button confirming the location of the new database.

Logging in

Each database is created containing a default project and two default user names: Administrator and Guest. Both of these user names are created with blank passwords that can be changed after the initial login.



Initially, choose Administrator from the drop down menu. The path for the active database is displayed at the bottom of the window. Once logged in, passwords and new users can be created from the Manage Users dialog under the Options menu.

ProteinChip® Software Quick Start

What's new in v3.0?

Database

Many of the enhancements to this version are enabled by using a database to store important information about the data. The database allows the software to build new experiments from existing spectra, and to sort and manage the spectra properties. These properties include the sample information associated with each spectra along with all of the ProteinChip® protocol conditions such as the type of ProteinChip array, the wash conditions and the data collection parameters. This arrangement makes it easy to construct experiments for the conditions that you wish to analyze, and will allow much greater flexibility with data management in future versions.

Biomarker Wizard

The Biomarker Wizard has been significantly enhanced. The important changes include:

- The output of Biomarker Wizard is now in a splitter window. The splitter window is saved along with the experiment, eliminating the need to rerun Biomarker Wizard. The mass range of the plot tracks the experiment.
- A Box and Whiskers plot is available to summarize complex biomarker patterns.
- The clustering now allows the use of manual peaks. This allows you to define the peaks of interest in a few spectra and then allow Biomarker Wizard to find or estimate the peaks for the remaining spectra.
- Peak clusters can be saved and reloaded to another experiment. This allows you to compare the same markers across multiple experiments.
- Biomarker Wizard can export data in a format compatible with the Biomarker Patterns Software.

Normalization

A new option in the normalization dialog allows normalizing to total ion current. This method generally reduces the average variation of spectra

across an experiment, and is the recommended default for expression profiling.

Signal Enhancement

A new option in the Filtering dialog enables a variable gain setting for high mass plus an additional filtering step. The combination improves the signal to noise ratio of high mass peaks. To use the feature, check the ‘Signal Enhance’ checkbox on the Filtering tab of the Analysis Protocol Properties.

Mass Calibration Equation

The form of the mass calibration has been changed from a cubic to a quadratic fit to allow calculating the high order coefficients with fewer calibration peaks. The mass accuracy of internal calibrations can be greatly improved over the linear defaults that the previous algorithm used.

Another significant improvement to the mass calibration is how calibrations are adjusted when using a single point calibration. Previous versions of the software required at least two points for an accurate mass calibration whereas this version will generate better calibrations with even a single internal standard.

Calibration Protocols

Calibration Protocols automate the process of mass calibration. The protocols contain a list of mass calibrants and rules that allow the software to identify the calibration peaks and generate a new mass calibration. This makes utilizing a mass standard such as the All-in-1 Peptide mix much easier. In addition, the calibration protocols can be applied to multiple spectra in an experiment, allowing you to align the mass of common peaks in a series of spectra from a protein profiling or other SELDI experiment.

Calibration Equations

The software now allows saving a calibration equation from a spectrum and applying calibration equations to one or more spectra.